Environmental cycle of antibiotic resistance encoded genes: A systematic review

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Abstract

Antibiotic-resistant bacteria and genes enter the environment in different ways. The release of these factors into the environment has increased concerns related to public health. The aim of the study was to evaluate the antibiotic resistance genes (ARGs) in the environmental resources. In this systematic review, the data were extracted from valid sources of information including ScienceDirect, PubMed, Google Scholar and SID. Evaluation and selection of articles were conducted on the basis of the PRISMA checklist. A total of 39 articles were included in the study, which were chosen from a total of 1249 papers. The inclusion criterion was the identification of genes encoding antibiotic resistance against the eight important groups of antibiotics determined by using the PCR technique in the environmental sources including municipal and hospital wastewater treatment plants, animal and agricultural wastes, effluents from treatment plants, natural waters, sediments, and drinking waters. In this study, 113 genes encoding antibiotic resistance to eight groups of antibiotics (beta-lactams, aminoglycosides, tetracyclines, macrolides, sulfonamides, chloramphenicol, glycopeptides and quinolones) were identified in various environments. Antibiotic resistance genes were found in all the investigated environments. The investigation of microorganisms carrying these genes shows that most of the bacteria especially gram-negative bacteria are effective in the acquisition and the dissemination of these pollutants in the environment. Discharging the raw wastewaters and effluents from wastewater treatments acts as major routes in the dissemination of ARGs into environment sources and can pose hazards to public health.

Keywords: Antibiotic resistance genes, Water and wastewater resources, Environmental pollution
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